



SEQUENCE ALIGNMENTS 1-3



SEQUENCE ALIGNMENT 1

	1	50
ADA89581	(1) MTKHYLNSKYQSEQRSSAMKKITMGTASIILGSLVYIGADSQQVNAATEA	
SEQ1	(1) -----	
	51	100
ADA89581	(51) TNATNNQSTOVSQATSQPINFQVKDGSSSEKSHMDDYMQHPGKVIKQNNK	
SEQ1	(1) -----MGTVQSQATSQPINFQVKDGSSSEKSHMDDYMQHPGKVIKQNNK	
	101	150
ADA89581	(101) YYFQTVLNNASFKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGY	
SEQ1	(45) YYFQTVLNNASFKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGY	
	151	200
ADA89581	(151) KSLTTKVHIVVPQINYNHRYTTHLEFEKAIPTLADAACKPNNVKPVQPKPA	
SEQ1	(95) KSLTTKVHIVVPQINYNHRYTTHLEFEKAIPTLADAACKPNNVKPVQPKPA	
	201	250
ADA89581	(201) QPKTPTEQTCKPVQPKVEVKVKPTVTTSKVEDNHSTKVVSTDTTKDQ-----	
SEQ1	(145) QPKTPTEQTCKPVQPKVEVKVKPTVTTSKVEDNHSTKVVSTDTTKDQTKTQ	
	251	300
ADA89581	(247) -----	
SEQ1	(195) TAHTVKTAQTAQEQNKVQTPVKDVATAKSESNNQAVSDNKSQQTNKVTKH	
	301	316
ADA89581	(247) -----	
SEQ1	(245) NETPKQASKAKELPKT	

SEQUENCE ALIGNMENT 2

SEQ1 AAU75475	(1) MGTQVSQATSQPINFQVQKDGSEKSHMDDYMQHPGKVIKQNNKYYFQTV (1) ----- 51	50 100
SEQ1 AAU75475	(51) LNNASFKEYKFYNANNQELATTVVNDNKKADTRTINVAVEPGYKSLTTK (1) ----- 101	150
SEQ1 AAU75475	(101) VHIVVPQINYNHRYTTHLEFEKAIPTLADAAPNNVKPVQPKPAQPKPTPT (1) ----- 151	200
SEQ1 AAU75475	(151) EQTKPVQPKVEVKPVTTSKVEDNHSTKVVSTD TTK DQTKTQTAHTVK (1) ----- 201	250
SEQ1 AAU75475	(201) TAQTAQEQNKVQTPVKDVATAKSESNNQAVSDNKSQOTNKVTKHNETPKQ (13) TAQTAQEQNKVQTPVKDVATAKSESNNQAVSDNKSQOTNKVTKHNETPKQ 251	294
SEQ1 AAU75475	(251) ASKAKELPKT (63) ASKAKELPKTGLTSVDNFISTVAFATLALLGSLSLLLFRKESK	

SEQUENCE ALIGNMENT 3

	1	50
ADA89548	(1) MTKHYLNSKYQSEQRSSAMKKITMGTASIILGSLVYIGADSQQVNAATEA	
SEQ1	(1) -----	
	51	100
ADA89548	(51) TNATNNQST <u>T</u> VSQATSQPINFOVQKDGSS <u>E</u> KSHMDDYMQHPGKV <u>I</u> KQNNK	
SEQ1	(1) ----- <u>MGT</u> VSQATSQPINFOVQKDGSS <u>E</u> KSHMDDYMQHPGKV <u>I</u> KQNNK	
	101	150
ADA89548	(101) YYFQTVLNNASF <u>W</u> KEYKFYNANN <u>Q</u> ELATTVVNDNKKADTRTINVAVEPGY	
SEQ1	(45) YYFQTVLNNASF <u>W</u> KEYKFYNANN <u>Q</u> ELATTVVNDNKKADTRTINVAVEPGY	
	151	200
ADA89548	(151) KSLTTKVHIVVPQINYNHRYTTHLEFEKAIP <u>L</u> ADA <u>A</u> KPNNVKPVQPKPA	
SEQ1	(95) KSLTTKVHIVVPQINYNHRYTTHLEFEKAIP <u>L</u> ADA <u>A</u> KPNNVKPVQPKPA	
	201	250
ADA89548	(201) QPKTPTEQT <u>K</u> PVQPKVE <u>V</u> KPTVTTSKVEDNHSTKVVSTD <u>T</u> TDQTKTQ	
SEQ1	(145) QPKTPTEQT <u>K</u> PVQPKVE <u>V</u> KPTVTTSKVEDNHSTKVVSTD <u>T</u> TDQTKTQ	
	251	300
ADA89548	(251) TAHTVKTA <u>Q</u> TA <u>Q</u> E <u>Q</u> NK <u>V</u> QTPVKDVATA <u>K</u> S <u>E</u> SNN <u>Q</u> AV <u>S</u> D <u>N</u> K <u>S</u> Q <u>O</u> TNKVTKH	
SEQ1	(195) TAHTVKTA <u>Q</u> TA <u>Q</u> E <u>Q</u> NK <u>V</u> QTPVKDVATA <u>K</u> S <u>E</u> SNN <u>Q</u> AV <u>S</u> D <u>N</u> K <u>S</u> Q <u>O</u> TNKVTKH	
	301	350
ADA89548	(301) NETPKQASKAKELPK <u>T</u> GLTSVDNFISTVA <u>F</u> ATLALL <u>G</u> SL <u>S</u> LLL <u>F</u> KR <u>K</u> E <u>S</u> K	
SEQ1	(245) NETPKQASKAKELPK <u>T</u> -----	